

SEQUENCE LISTING

<110> Ian Popoff
Jacqueline Wyatt

<120> ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1, P127
EXPRESSION

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Met Ser Tyr Asn Tyr

1 5

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Val Val Thr Ala Gln Lys Pro Thr Ala Val Asn Gly Cys Val Thr Gly
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His Phe Thr Ser Ala Glu Asp Leu Asn Leu Leu Ile Ala Lys Asn Thr
25 30 35aga tta gag atc tat gtg gtc acc gcc gag ggg ctt cgg ccc gtc aaa 259
Arg Leu Glu Ile Tyr Val Val Thr Ala Glu Gly Leu Arg Pro Val Lys
40 45 50gag gtg ggc atg tat ggg aag att gcg gtc atg gag ctt ttc agg ccc 307
Glu Val Gly Met Tyr Gly Lys Ile Ala Val Met Glu Leu Phe Arg Pro
55 60 65aag ggg gag agc aag gac ctg ctg ttt atc ttg aca gcg aag tac aat 355
Lys Gly Glu Ser Lys Asp Leu Leu Phe Ile Leu Thr Ala Lys Tyr Asn
70 75 80 85gcc tgc atc ctg gag tat aaa cag agt ggc gag agc att gac atc att 403
Ala Cys Ile Leu Glu Tyr Lys Gln Ser Gly Glu Ser Ile Asp Ile Ile
90 95 100acg cga gcc cat ggc aat gtc cag gac cgc att ggc cgc ccc tca gag 451
Thr Arg Ala His Gly Asn Val Gln Asp Arg Ile Gly Arg Pro Ser Glu
105 110 115

acc ggc att att ggc atc att gac cct gag tgc cgg atg att ggc ctg 499
 Thr Gly Ile Ile Gly Ile Ile Asp Pro Glu Cys Arg Met Ile Gly Leu
 120 125 130

cgt ctc tat gat ggc ctt ttc aag gtt att cca cta gat cgc gat aat 547
 Arg Leu Tyr Asp Gly Leu Phe Lys Val Ile Pro Leu Asp Arg Asp Asn
 135 140 145

aaa gaa ctc aag gcc ttc aac atc cgc ctg gag gag ctg cat gtc att 595
 Lys Glu Leu Lys Ala Phe Asn Ile Arg Leu Glu Glu Leu His Val Ile
 150 155 160 165

gat gtc aag ttc cta tat ggt tgc caa gca cct act att tgc ttt gtc 643
 Asp Val Lys Phe Leu Tyr Gly Cys Gln Ala Pro Thr Ile Cys Phe Val
 170 175 180

tac cag gac cct cag ggg cgg cac gta aaa acc tat gag gtg tct ctc 691
 Tyr Gln Asp Pro Gln Gly Arg His Val Lys Thr Tyr Glu Val Ser Leu
 185 190 195

cga gaa aag gaa ttc aat aag ggc cct tgg aaa cag gaa aat gtc gaa 739
 Arg Glu Lys Glu Phe Asn Lys Gly Pro Trp Lys Gln Glu Asn Val Glu
 200 205 210

gct gaa gct tcc atg gtg atc gca gtc cca gag ccc ttt ggg ggg gcc 787
 Ala Glu Ala Ser Met Val Ile Ala Val Pro Glu Pro Phe Gly Gly Ala
 215 220 225

atc atc att gga cag gag tca atc acc tat cac aat ggt gac aaa tac 835
 Ile Ile Ile Gly Gln Glu Ser Ile Thr Tyr His Asn Gly Asp Lys Tyr
 230 235 240 245

ctg gct att gcc cct cct atc atc aag caa agc acg att gtg tgc cac 883
 Leu Ala Ile Ala Pro Pro Ile Ile Lys Gln Ser Thr Ile Val Cys His
 250 255 260

aat cga gtg gac cct aat ggc tca aga tac ctg ctg gga gac atg gaa 931
 Asn Arg Val Asp Pro Asn Gly Ser Arg Tyr Leu Leu Gly Asp Met Glu
 265 270 275

ggc cgg ctc ttc atg ctg ctt ttg gag aag gag gaa cag atg gat ggc 979
 Gly Arg Leu Phe Met Leu Leu Leu Glu Lys Glu Glu Gln Met Asp Gly
 280 285 290

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 Thr Val Thr Leu Lys Asp Leu Arg Val Glu Leu Leu Gly Glu Thr Ser
 295 300 305

att gct gag tgc ttg aca tac ctt gat aat ggt gtt gtg ttt gtc ggg 1075
 Ile Ala Glu Cys Leu Thr Tyr Leu Asp Asn Gly Val Val Phe Val Gly
 310 315 320 325

tct cgc ctg ggt gac tcc cag ctt gtg aag ctc aac gtt gac agt aat 1123
 Ser Arg Leu Gly Asp Ser Gln Leu Val Lys Leu Asn Val Asp Ser Asn
 330 335 340

gaa caa ggc tcc tat gta gtg gcc atg gaa acc ttt acc aac tta gga 1171
 Glu Gln Gly Ser Tyr Val Val Ala Met Glu Thr Phe Thr Asn Leu Gly
 345 350 355

ccc att gtc gat atg tgc gtg gtg gac ctg gag agg cag ggg cag ggg 1219
 Pro Ile Val Asp Met Cys Val Val Asp Leu Glu Arg Gln Gly Gln Gly
 360 365 370

cag ctg gtc act tgc tct ggg gct ttc aag gaa ggt tct ttg cgg atc 1267
 Gln Leu Val Thr Cys Ser Gly Ala Phe Lys Glu Gly Ser Leu Arg Ile
 375 380 385

atc cgg aat gga att gga atc cac gag cat gcc agc att gac tta cca 1315
 Ile Arg Asn Gly Ile Gly Ile His Glu His Ala Ser Ile Asp Leu Pro
 390 395 400 405

ggc atc aaa gga tta tgg cca ctg cgg tct gac cct aat cgt gag act 1363
 Gly Ile Lys Gly Leu Trp Pro Leu Arg Ser Asp Pro Asn Arg Glu Thr
 410 415 420

gat gac act ttg gtg ctc tct ttt gtg ggc cag aca aga gtt ctc atg 1411
 Asp Asp Thr Leu Val Leu Ser Phe Val Gly Gln Thr Arg Val Leu Met
 425 430 435

tta aat gga gag gag gta gaa gaa acc gaa ctg atg ggt ttc gtg gat 1459
 Leu Asn Gly Glu Glu Val Glu Glu Thr Glu Leu Met Gly Phe Val Asp
 440 445 450

gat cag cag act ttc ttc tgt ggc aac gtg gct cat cag cag ctt atc 1507
 Asp Gln Gln Thr Phe Phe Cys Gly Asn Val Ala His Gln Gln Leu Ile
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003001-25111600

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 Gln Ile Thr Ser Ala Ser Val Arg Leu Val Ser Gln Glu Pro Lys Ala
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ctg gtc agt gaa tgg aag gag cct cag gcc aag aac atc agt gtg gcc 1603
 Leu Val Ser Glu Trp Lys Glu Pro Gln Ala Lys Asn Ile Ser Val Ala
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tcc tgc aat agc agc cag gtg gtg gtg gct gta ggc agg gcc ctc tac 1651
 Ser Cys Asn Ser Ser Gln Val Val Val Ala Val Gly Arg Ala Leu Tyr
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tat ctg cag atc cat cct cag gag ctc cgg cag atc agc cac aca gag 1699
 Tyr Leu Gln Ile His Pro Gln Glu Leu Arg Gln Ile Ser His Thr Glu
 520 525 530

atg gaa cat gaa gtg gct tgc ttg gac atc acc cca tta gga gac agc 1747
 Met Glu His Glu Val Ala Cys Leu Asp Ile Thr Pro Leu Gly Asp Ser
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aat gga ctg tcc cct ctt tgt gcc att ggc ctc tgg acg gac atc tcg 1795
 Asn Gly Leu Ser Pro Leu Cys Ala Ile Gly Leu Trp Thr Asp Ile Ser
 550 555 560 565

gct cgt atc ttg aag ttg ccc tct ttt gaa cta ctg cac aag gag atg 1843
 Ala Arg Ile Leu Lys Leu Pro Ser Phe Glu Leu Leu His Lys Glu Met
 570 575 580

ctg ggt gga gag atc att cct cgc tcc atc ctg atg acc acc ttt gag 1891
 Leu Gly Gly Glu Ile Ile Pro Arg Ser Ile Leu Met Thr Thr Phe Glu
 585 590 595

agt agc cat tac ctc ctt tgt gcc ttg gga gat gga gcg ctt ttc tac 1939
 Ser Ser His Tyr Leu Leu Cys Ala Leu Gly Asp Gly Ala Leu Phe Tyr
 600 605 610

ttt ggg ctc aac att gag aca ggt ctg ttg agc gac cgt aag aag gtg 1987
 Phe Gly Leu Asn Ile Glu Thr Gly Leu Leu Ser Asp Arg Lys Lys Val
 615 620 625

act ttg ggc acc cag ccc acc gta ttg agg act ttt cgt tct ctt tct 2035
 Thr Leu Gly Thr Gln Pro Thr Val Leu Arg Thr Phe Arg Ser Leu Ser
 630 635 640 645

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agc	aac	cac	aaa	ttg	gtc	ttc	tca	aat	gtc	aac	ctc	aag	gaa	gtg	aac	2131
Ser	Asn	His	Lys	Leu	Val	Phe	Ser	Asn	Val	Asn	Leu	Lys	Glu	Val	Asn	
				665				670					675			
tac	atg	tgt	ccc	ctc	aat	tca	gat	ggc	tat	cct	gac	agc	ctg	gcg	ctg	2179
Tyr	Met	Cys	Pro	Leu	Asn	Ser	Asp	Gly	Tyr	Pro	Asp	Ser	Leu	Ala	Leu	
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gcc	aac	aat	agc	acc	ctc	acc	att	ggc	acc	atc	gat	gag	atc	cag	aag	2227
Ala	Asn	Asn	Ser	Thr	Leu	Thr	Ile	Gly	Thr	Ile	Asp	Glu	Ile	Gln	Lys	
				695			700					705				
ctg	cac	att	cgc	aca	gtt	ccc	ctc	tat	gag	tct	cca	agg	aag	atc	tgc	2275
Leu	His	Ile	Arg	Thr	Val	Pro	Leu	Tyr	Glu	Ser	Pro	Arg	Lys	Ile	Cys	
710					715					720					725	
tac	cag	gaa	gtg	tcc	cag	tgt	ttc	ggg	gtc	ctc	tcc	agc	cgc	att	gaa	2323
Tyr	Gln	Glu	Val	Ser	Gln	Cys	Phe	Gly	Val	Leu	Ser	Ser	Arg	Ile	Glu	
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gtc	caa	gac	acg	agt	ggg	ggc	acg	aca	gcc	ttg	agg	ccc	agc	gct	agc	2371
Val	Gln	Asp	Thr	Ser	Gly	Gly	Thr	Thr	Ala	Leu	Arg	Pro	Ser	Ala	Ser	
				745				750					755			
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Thr	Gln	Ala	Leu	Ser	Ser	Ser	Val	Ser	Ser	Ser	Lys	Leu	Phe	Ser	Ser	
				760				765					770			
agc	act	gct	cct	cat	gag	acc	tcc	ttt	gga	gaa	gag	gtg	gag	gtg	cac	2467
Ser	Thr	Ala	Pro	His	Glu	Thr	Ser	Phe	Gly	Glu	Glu	Val	Glu	Val	His	
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aac	cta	ctt	atc	att	gac	caa	cac	acc	ttt	gaa	gtg	ctt	cat	gcc	cac	2515
Asn	Leu	Leu	Ile	Ile	Asp	Gln	His	Thr	Phe	Glu	Val	Leu	His	Ala	His	
790					795					800					805	
cag	ttt	ctg	cag	aat	gaa	tat	gcc	ctc	agt	ctg	gtt	tcc	tgc	aag	ctg	2563
Gln	Phe	Leu	Gln	Asn	Glu	Tyr	Ala	Leu	Ser	Leu	Val	Ser	Cys	Lys	Leu	
				810					815					820		

Parameter	Value	Unit	Source
Age	25.0	yr	Mean
Height	1.75	m	Mean
Weight	70.0	kg	Mean
BMI	22.2	kg/m ²	Mean
Heart rate	75	beats/min	Mean
Stroke volume	70	ml	Mean
Cardiac output	5.25	l/min	Mean
Systemic blood pressure	120/80	mmHg	Mean
Pulmonary artery pressure	25/15	mmHg	Mean
Pulmonary capillary pressure	15/10	mmHg	Mean
Left ventricular pressure	120/80	mmHg	Mean
Right ventricular pressure	25/15	mmHg	Mean
Left ventricular stroke volume	70	ml	Mean
Right ventricular stroke volume	70	ml	Mean
Left ventricular stroke work	1.05	J	Mean
Right ventricular stroke work	0.15	J	Mean
Left ventricular stroke power	1.05	W	Mean
Right ventricular stroke power	0.15	W	Mean
Left ventricular stroke efficiency	0.25		Mean
Right ventricular stroke efficiency	0.25		Mean
Left ventricular stroke volume index	40	ml/m ²	Mean
Right ventricular stroke volume index	40	ml/m ²	Mean
Left ventricular stroke work index	0.05	J/m ²	Mean
Right ventricular stroke work index	0.01	J/m ²	Mean
Left ventricular stroke power index	0.05	W/m ²	Mean
Right ventricular stroke power index	0.01	W/m ²	Mean
Left ventricular stroke efficiency index	0.25		Mean
Right ventricular stroke efficiency index	0.25		Mean
Left ventricular stroke volume index	40	ml/m ²	Mean
Right ventricular stroke volume index	40	ml/m ²	Mean
Left ventricular stroke work index	0.05	J/m ²	Mean
Right ventricular stroke work index	0.01	J/m ²	Mean
Left ventricular stroke power index	0.05	W/m ²	Mean
Right ventricular stroke power index	0.01	W/m ²	Mean
Left ventricular stroke efficiency index	0.25		Mean
Right ventricular stroke efficiency index	0.25		Mean

ggc aaa gac ccc aac act tac ttc att gtg ggc aca gca atg gtg tat 2611
 Gly Lys Asp Pro Asn Thr Tyr Phe Ile Val Gly Thr Ala Met Val Tyr
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cct gaa gag gca gag ccc aag cag ggt cgc att gtg gtc ttt cag tat 2659
 Pro Glu Glu Ala Glu Pro Lys Gln Gly Arg Ile Val Val Phe Gln Tyr
 840 845 850

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 Ser Asp Gly Lys Leu Gln Thr Val Ala Glu Lys Glu Val Lys Gly Ala
 855 860 865

gtg tac tct atg gtg gaa ttt aac ggg aag ctg tta gcc agc atc aat 2755
 Val Tyr Ser Met Val Glu Phe Asn Gly Lys Leu Leu Ala Ser Ile Asn
 870 875 880 885

agc acg gtg cgg ctc tat gag tgg aca aca gag aag gag ctg cgc act 2803
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 890 895 900

gag tgc aac cac tac aac aac atc atg gcc ctc tac ctg aag acc aag 2851
 Glu Cys Asn His Tyr Asn Asn Ile Met Ala Leu Tyr Leu Lys Thr Lys
 905 910 915

ggc gac ttc atc ctg gtg ggc gac ctt atg cgc tca gtg ctg ctg ctt 2899
 Gly Asp Phe Ile Leu Val Gly Asp Leu Met Arg Ser Val Leu Leu Leu
 920 925 930

gcc tac aag ccc atg gaa gga aac ttt gaa gag att gct cga gac ttt 2947
 Ala Tyr Lys Pro Met Glu Gly Asn Phe Glu Glu Ile Ala Arg Asp Phe
 935 940 945

aat ccc aac tgg atg agt gct gtg gaa atc ttg gat gat gac aat ttt 2995
 Asn Pro Asn Trp Met Ser Ala Val Glu Ile Leu Asp Asp Asp Asn Phe
 950 955 960 965

ctg ggg gct gaa aat gcc ttt aac ttg ttt gtg tgt caa aag gat agc 3043
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 970 975 980

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 Ala Ala Thr Thr Asp Glu Glu Arg Gln His Leu Gln Glu Val Gly Leu
 985 990 995

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Phe His Leu Gly Glu Phe Val Asn Val Phe Cys His Gly Ser Leu Val	
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atg cag aat ctg ggt gag act tcc acc ccc aca caa ggc tgc gtg ctc	3187
Met Gln Asn Leu Gly Glu Thr Ser Thr Pro Thr Gln Gly Ser Val Leu	
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ttc ggc acg gtc aac ggc atg ata ggg ctg gtg acc tca ctg tca gag	3235
Phe Gly Thr Val Asn Gly Met Ile Gly Leu Val Thr Ser Leu Ser Glu	
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agc tgg tac aac ctc ctg ctg gac atg cag aat cga ctc aat aaa gtc	3283
Ser Trp Tyr Asn Leu Leu Leu Asp Met Gln Asn Arg Leu Asn Lys Val	
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atc aaa agt gtg ggg aag atc gag cac tcc ttc tgg aga tcc ttt cac	3331
Ile Lys Ser Val Gly Lys Ile Glu His Ser Phe Trp Arg Ser Phe His	
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acc gag cgg aag aca gaa cca gcc aca ggt ttc atc gac ggt gac ttg	3379
Thr Glu Arg Lys Thr Glu Pro Ala Thr Gly Phe Ile Asp Gly Asp Leu	
1080 1085 1090	
att gag agt ttc ctg gat att agc cgc ccc aag atg cag gag gtg gtg	3427
Ile Glu Ser Phe Leu Asp Ile Ser Arg Pro Lys Met Gln Glu Val Val	
1095 1100 1105	
gca aac cta cag tat gac gat ggc agc ggt atg aag cga gag gcc act	3475
Ala Asn Leu Gln Tyr Asp Asp Gly Ser Gly Met Lys Arg Glu Ala Thr	
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gca gac gac ctc atc aag gtt gtg gag gag cta act cgg atc cat tag	3523
Ala Asp Asp Leu Ile Lys Val Val Glu Glu Leu Thr Arg Ile His	
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